REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 16, 17, and 23-25 have been amended. No new matter is being presented, and approval and entry are respectfully requested.

Claims 16-17 and 23-25 are under consideration. Claim 26 is withdrawn. Reconsideration is respectfully requested.

WITHDRAWAL OF CLAIM 26:

Claim 26 was withdrawn as being directed to an invention that is independent or distinct from the invention originally claimed.

REJECTION UNDER 35 U.S.C. §102:

In the Office Action, at pages 3-4 and in the Response to Arguments on pages 6-7, claims 16, 17 and 23-25 were rejected under 35 U.S.C. §102(b) as being anticipated by Pantoliano et al. (USPN 4,853,871; hereafter, Pantoliano) or Holak et al. (J. Mol., 210, 653-648; hereafter, Holak) or Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045; hereafter, Flaherty) or Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992; hereafter, Mosimann). This rejection is traversed and reconsideration is requested.

Claims 16-17 and 23-25 have been amended for clarity.

The Examiner submitted that claims 16-17 and 23-25 read on any reference teaching comparison of two three-dimensional structures and calculating RMSD therefor.

Independent claim 16 has been amended to show more clearly that the present claimed invention recites a comparison of secondary structures of a probe structure and a target structure, wherein a first subset of a secondary structure of the probe structure is compared with a second subset of a secondary structure of the target structure using a tree pruning structure, an attribute determination, and an RMSD determination to generate a longest common subsequence.

Hence, claim 16 provides a method of determining spatially similar portions of substances by analyzing three-dimensional structures of ~~the~~ a ~~substances~~ substance ~~including~~ by comparing a first probe structure expressed by three-dimensional coordinates of elements belonging to a first subset of a plurality of subsets of secondary structures of probe structures, the first subset comprising a first point set of an amino acid sequence database or a motif database and a second target structure expressed by three-dimensional coordinates of elements belonging to a second subset of a plurality of subsets of secondary structures of the

target structure, the second subset comprising a second point set of an input amino acid sequence of the target structure, comprising:

dividing the second structure into a plurality of second subsets based on secondary structures of the three-dimensional coordinates of the target structure;

~~dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets;~~

determining whether a correspondence is present between the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure by, for each subset of the plurality of subsets of secondary structures of the target structure:

generating a first tree structure for the first point set of the probe structure and a second tree structure for the second point set of the target structure;

pruning the second tree structure for the second point set of the plurality of second subsets of the target structure in accordance with a predetermined pruning procedure; and

determining whether the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure have a same attribute, and if the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure have a same attribute, generating a correspondence between the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure; and

~~generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence;~~

~~determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and~~

calculating a root mean square distance (RMSD) between ~~all of the~~ elements corresponding in the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure ~~the optimum correspondence~~ to automatically determine a distance between the elements of the first point set and the elements of the second point set;

determining whether the RMSD is less than or equal to a predetermined threshold value, and where the RMSD is less than or equal to a predetermined threshold value, generating an optimum correspondence between the first point set of the probe structure and the second point set of the plurality of second subsets of the target structure; ~~that have an optimal~~

~~correspondence~~ and

~~to determine~~determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having ~~a greatest~~the optimum correspondence to the input amino acid sequence.

Independent claims 23 and 24 have been amended similarly.

It is respectfully submitted that the courts have held: "Anticipation requires a lack of novelty of the invention as claimed. The invention must have been known to the art in the detail of the claim; that is, all of the elements and limitations of the claim must be shown in a single prior reference, arranged as in the claim." See C.R. Bard, Inc. v. M3 Systems, Inc., 157 F3d 1340, 1349, 48 USPQ2d 1225, 1229-30 (Fed. Cir. 1998); Richardson v. Suzuki Motor Co., 868 F.2d 1226, 1236, 9 USPQ2d 1913, 1920 (Fed. Cir. 1989).

Pantoliano recites, in claim 1:

> 1. A computer based method for evaluating a protein's structure to determine whether said protein contains at least two target amino acid residues, replacement of at least one of which with a cysteine residue would be sufficient to **permit formation of at least one potentially protein-stabilizing disulfide bond**; said method comprising the steps:
>
> (1) examining each selected pair of amino acid residues in said protein to determine if they contain certain atoms whose relative three-dimensional positions possess a geometric conformation similar to a geometric conformation possessed by atoms of a **disulfide bond**,
>
> (2) examining any pair of amino acids found to contain said certain atoms identified in step (1) to determine **whether said disulfide bond can be accommodated without** creating unacceptable **steric hindrance**,
>
> (3) permitting an expert operator (i) to view any possible **disulfide bond** which can be accommodated without creating unacceptable steric hindrance, and (ii) to rank said viewed **possible disulfide bond** from most **likely to stabilize an engineered protein** to least likely to stabilize said protein, and
>
> (4) **evaluating said ranked possible disulfide bond** according to expert rule criterion.
>
> (emphasis added)

Hence, it is respectfully submitted that Pantoliano recites a method of determining whether a disulfide bond may be accommodated in an engineered protein, and does not recite the elements of amended independent claim 16, 23 or 24 of the present invention. Hence, amended independent claims 16, 23 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871). Since claims 17 and 25 depend from amended claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871) for at least the reasons that

amended claims 16 and 24 are not anticipated under 35 U.S.C. §102(b) by Pantoliano et al. (USPN 4,853,871).

Holak discloses determination of a three dimensional structure of the trypsin inhibitor from squash seeds in aqueous solution by **nuclear magnetic resonance** and a **combination of distance geometry and dynamical simulated annealing** (see Abstract, Holak et al.). However, Holak et al. does not recite the elements of amended independent claim 16, 23 or 24 of the present invention. Hence, amended independent claims 16, 23 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol., 210, 653-648). Since claims 17 and 25 depend from amended claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol., 210, 653-648) for at least the reasons that amended claims 16 and 24 are not anticipated under 35 U.S.C. §102(b) by Holak et al. (J. Mol., 210, 653-648).

Flaherty discloses **using a rmsd and a "fingerprint"** to determine similarity of the three-dimensional structures of actin and the ATPase fragment of a 70-kDa heat shock cognate protein, noting that the structural differences between the two molecules mainly occur in loop regions of actin known to be involved in interactions with other monomers in the actin filament or in the binding of myosin (see Abstract, Flaherty et al.). However, Flaherty does not recite the elements of amended independent claim 16, 23 or 24 of the present invention. Hence, amended independent claims 16, 23 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045). Since claims 17 and 25 depend from amended claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045) for at least the reasons that amended claims 16 and 24 are not anticipated under 35 U.S.C. §102(b) by Flaherty et al. (Proc. Natl. Acad. Sci. USA, 88, 5041-5045).

Mosimann discloses a comparative molecular model of P-30 protein constructed **based on the known three-dimensional structure of bovine pancreatic RNase**, wherein, in the **modeling procedure**, **automatic sequence alignments were revised based upon** the **inspection of the RNase A structure before the amino acids of the P-30 protein were assigned the coordinates of the RNase A template**, **intermolecular steric clashes were relieved** on an interactive graphics device through the **adjustment of side chain torsion angles**, and **energy minimizing** of the model to optimize stereochemistry and relieve any remaining unacceptably close contacts (see Abstract, Mosimann et al.). However, Mosimann et al. does not recite the elements of amended independent claim 16, 23 or 24 of the present invention. Hence, amended independent claims 16, 23 and 24 are submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and

Genetics, 14, 392-400, 1992). Since claims 17 and 25 depend from amended claims 16 and 24, respectively, claims 17 and 25 are submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992) for at least the reasons that amended claims 16 and 24 are not anticipated under 35 U.S.C. §102(b) by Mosimann et al. (Proteins: Structure, Function and Genetics, 14, 392-400, 1992).

DOUBLE PATENTING:

Claims 16, 17 and 23 were provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claim 13 of copending Application No. 09/910,071.

On pages 4-6 of the Office Action, the Examiner provisionally rejects claims 16, 17 and 23 under the judicially created doctrine of obviousness-type double patenting in view of claim 13 of copending U.S. Patent Application No. 09/910,071. Since U.S. Patent Application No. 09/910,071 has not yet been issued as a patent, and since the all of the claims of the instant application have not yet been indicated as allowable except for the provisional rejection, it is believed that any submission of a Terminal Disclaimer or arguments as to the non-obvious nature of the claims would be premature. MPEP 804(I)(B). As such, it is respectfully requested that the applicants be allowed to address any obviousness-type double patenting issues remaining once the rejection of the claims under 35 U.S.C. §103 is resolved or on allowance of U.S. Patent Application No. 09/910,071.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited by the Examiner contacting the undersigned attorney for a telephone interview to discuss resolution of such issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

STAAS & HALSEY LLP

Date: March 6, 2006 By: Darleen J. Stockley

Darleen J. Stockley
Registration No. 34,257

1201 New York Avenue, N.W.
Suite 700
Washington, D.C. 20005
Telephone: (202) 434-1500
Facsimile: (202) 434-1501